

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGC  
 GAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGTCCTCAGGGACGACTCTGCCATC  
 GAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAG  
 AAAAGTTCTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACCCGAGGACGTTCCGGCAATC  
 CGCGACAAAATAAGGAAGCACCCCGCGGTCTATCGACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTAC  
 CTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGACATCGAGACG  
 CTCTACCACGAGGGAGAAGAGTTTGGAAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCG  
 CGCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAG  
 CGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGAGCTGTGATAACATAACCGCGACAACCTTCGACTTC  
 GCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCCCTCGGGAGGGACGGGAGCGAGCCGAAG  
 ATACAGCGCATGGGGGACAGGTTTGGCGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATA  
 AGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAG  
 AAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCG  
 ATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTC  
 ATCGGCCAAGGCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCTTAAGGAAG  
 GCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTAC  
 gcCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGATCTAGACTTTCGTAGTCTC  
 TACCTTCAATCATAATCACCCACAACGTCCTCGCCAGATACGCTCAACCGCGAGGGGTGTAGGAGTACGAC  
 GTTGCCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCCGAGCCTGTCTCGGAAACCTG  
 CTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGAT  
 TACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCAGGGCAAGATGG  
 TACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTT  
 GAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCTTGAGCGGAC  
 GCTGAAACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAAGTGGCCGCTTCTCGAA  
 CTCGAATACGAGGGCTTCTACGTACAGGGGCTTCTTCGTACGAAAGAAAAGTACGCGGTCTACGACGAGGAG  
 GGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGGACTGGAGCGAGATAGCGAAGGAGACGCAGGCG  
 AGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCGTCAGAATTGTCAGGGAAGTCACCGAA  
 AAGCTGAGCAAGTACGAGGTTCCGCCGAGAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGAC  
 TACAAGGCCACCGCCCGCACGTAGCCATAGCGAAgcGTTTGGCCGCCAGAGGTGTTAAATCCGGCCCGGA  
 ACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTC  
 GACCCGACGAAGCACAACTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGCGAGTTGAGAGAATC  
 CTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTGGGGCTTGGCGCGTGG  
 CTGAAGCCGAAGGGGAAGAAGAAGTGA

FIG. 1

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVRAEKVK  
KKFLGRSVEVWVLYFTHPQDVPARDKIRKHPAVIDIYEDIPFAKRYLIDKGLIPMEGEEELKLMSFDIET  
LYHEGEEFGTGPILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDLITYNGDNFDF  
AYLKKRCEKLGVSFTLGRDGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKE  
KVYAEIATAWETGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRK  
AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYD  
VAPEVGHKFKCDFPGFIPSLGNLLEERQKIKRKMATLDPLEKNLLDYRQRAIKILANSYGYGYARARW  
YCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLE  
LEYEGFYVRGFFVTKKKYAVIDEKGKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTE  
KLSKYEVPPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPDEF  
DPTKHKYDADYYIENQVLPAYERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

FIG. 2

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDS AIEE  
 IKKITAERHGRVVKVRAEKVKKKFLGRSVEVWVLYFTHPQDVP AIRDKI  
 RKHPAVIDIY EYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGE  
 EFGTGPILMISYADESEARVITWKKIDLPYVEVVS TEKEMIKRFLRVVKE  
 KDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGRD GSEP KIQRMGDRFAV Extein 1  
 EVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVY AEEIATAWE  
 TGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSR SSTG  
 NLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNI  
 VYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKCKDFPGFIP  
 SLLGNLLEERQKIKRKMKATLDPLEKNLLDYRQRAIKILAN

SLLPGEWVA  
 VIEGGKLRPV RIGELVDGLMEASGERVKRDGDTEVLEVEGLYAS PSTGSP  
 RKPAQCR\*KP\*\*GTAMPGKFTE\*LSTPEGGLSVTRGHS LFAYRDASLWR\*  
 RGRRRFKPGDLLAVPSG\*PSRRGGRGSTSLNCSSNCPRRKRPTCHRHSGK  
 GRKNFFRGMRLRTLWIFGEEKTGGRPGATWSTLRGLGYVKLRKIGYGVVD  
 REGLGKVPFRFYERLVEVIRYNGNRGEFIADFNALRPVLR LMMPEKELEEW Intein 1  
 LVGTRNGFRIRPFIEVDWKFAKLLGYVYVSEGSAGKWK NRTGGWSYSVRLY  
 NEDGSVLDDMERLARSSLGA\*ARGELRRDFKEDGLHNLRGALRFTGREQE  
 GSVAYLHVP\*GGPLGLP\*GVLHRRRRRSPEQDGSALHQERASG\*RPRPAP  
 ELAGRLSDKRPPRQRLQGLRERGTALYRVPEAEERLTYSHVIPREVLEE  
 TSAGPSRRT\*VTGNSGSWWKAGSSTRKGPVG\*AGSSTGI\*SSTGSRKSGR  
 KATRGTTST\*ALRRTRTSGGLWVPLRAQX

SYYGYYGYARARWYCRECAES  
 VTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAME  
 FLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDE EGKITTRGLEIVR  
 RDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVI Extein 2  
 HEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYIVLKGSGRIGD  
 RAIPFDEFDPTKHKYDADYYIENQVLP AVERILRAFGYRKEDLRYQKTRQ  
 VGLGAWLKPKGKKK

FIG. 3

AATTCCACTGCCGTGTTTAACTTTCCACCGTTGAACTTGAGGGTGATTT  
 TCTGAGCCTCCTCAATCACTTAATCGAGACCGCGGATTACCTTGAACGG  
 TACACGTTCAACGATTCGGTTCCTGTAATGGTCGATACTGGGCCGTGCTG  
 GATTTTCTAAACGTCTCAAGAACGGCTTTTCATCAACGGAACTGCCACGT 5' untranslated sequence  
 CTCCGCCGTCGTGAGGGTTAAACCTGAAGTTCAAGACTTTGCAACGGAAT  
 GCGGAGAGAACGGCGACTACCCAGTGAAGAGCTTTTGAAAGCCAAAGC  
 CGAGCTTCAGCGAATGTGCGGTGCCCTTGTTCAAGAGTTGTGAGCCCTTG  
 ATTGTTGTTTTCTCCTCTTTTCTGATAACATCGATGGCGAAGTTATTAG  
 TTCTCAGTTCGATAATCAGGCAGGTGTTGGTC

ATGATCCTTGACGTTGAT  
 TACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAA  
 CGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACG  
 CGTCTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCG  
 GAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAA  
 AAAGTTCCTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACC  
 CGCAGGACGTTCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGTG  
 ATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGA  
 CAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAACTCATGTCTT  
 TCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGAACCGGGCCG  
 ATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTG  
 GAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGA  
 TGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTG  
 ATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTG  
 TGAGAAGCTTGGCGTGAGCTTTACCTCGGGAGGGACGGGAGCGAGCCGA Extein 1  
 AGATACAGCGCATGGGGGACAGGTTTGCGGTGAGGTGAAGGGCAGGGTA  
 CACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTA  
 CACCCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAGAAGG  
 TCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAG  
 AGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGG  
 CAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAG  
 GCCTCTGGGACGTTTCCCGCTCCAGCACCGCAACCTCGTCGAGTGGTTC  
 CTCTTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGA  
 CGAGAGGGAGCTGGCGAGGAGAAGGGGGGCTACGCCGGTGGCTACGTCA  
 AGGAGCCCGAGCGGGGACTGTGGGACAATATCGTGATCTAGACTTTCGT  
 AGTCTCTACCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCT  
 CAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCGAGGTCGGTCACA  
 AGTTCGTCAAGGACTTCCCGGCTTCATTCCGAGCCTGCTCGGAAACCTG  
 CTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCC  
 GCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCG  
 CCAAC

FIG. 4

AGCCTTCTTCCCGGGAGTGGGTTCGGGTCATTGAAGGGGGGAAA  
 CTCAGGCCCGTCCGCATCGGCGAGCTGGTTGATGGACTGATGGAAGCCAG  
 CGGGGAGAGGGTGAAAAGAGACGGCGACACCGAGGTCCCTTGAAGTCGAGG  
 GGCTTTACGCCTCTCCTTCGACAGGGAGTCCAAGAAAGCCCGCACAATGC  
 CGGTGAAAGCCGTGATAAGGCACCGCTATGCCGGGAAGTTTACAGAATA  
 GCTCTCAACTCCGGAAGGAGGATTAAGCGTGACGCGCGGCCACAGCCTCT  
 TCGCGTACCGGGACGCGAGCTTGTGGAGGTGACGGGGGAGGAGGAGGTTT  
 AAGCCCGGCGACCTCCTGGCGGTGCCAAGCGGATAACCCTCCCGGAGAGG  
 AGGGAGAGGCTCAACATCGTTGAACTGCTCCTCGAACTGCCCCGAGGAGGA  
 AACGGCCGACATGTCATCGACATTCCGGCAAGGGTAGAAAGAACTTCTTC  
 AGGGGAATGCTCAGAACCTCCGCTGGATTTTCGGGAGGAGAAGACCGG Intein 1  
 AGGGCGGCCAGGCGCTACCTGGAGCACCTTGCCTGGGCTCGGCTACGTGA  
 AGCTGAGGAAAATCGGCTACGGGGTGGTTGATAGGAGGGACTGGGAAAG  
 GTACCGCGCTTCTACGAGAGGCTCGTGGAGGTAATCCGCTACAACGGCAA  
 CAGGGGGGAGTTCATCGCCGATTTC AACGCGCTCCGCCCCGTCTCCGCC  
 TGATGATGCCCGAGAAGGAGCTTGAAGAGTGGCTCGTTGGGACGAGGAAC  
 GGGTTTCAGGATAAGGCCGTTTCATAGAGGTTGATTGGAAGTTTCGAAAGCT  
 CCTCGGCTACTACGTGAGCGAGGGGAGCGCCGGGAAGTGGA AAAACCGGA  
 CCGGGGGCTGGAGCTACTCGGTGAGGCTTTACAACGAGGACGGGAGCGTT  
 CTCGACGACATGGAGAGACTCGCGAGGAGTTCTTTGGGGCGTGAGCGCG  
 GGGGGAAC TACGTCGAGATTTCAAAGAAGATGGCCTACATAATCTTCGAG  
 GGGCTCTGCGGTTACCGGCCGAGAACAAGAGGGTTCCGTGGCTTATCTT  
 CACGTCCCCTGAGGAGGTCCGCTGGGCCTTCCTTGAGGGGTACTTCATCG  
 GCGACGGCGACGTTCACCCGAGCAAGATGGTTCCGGCTCTCCACCAAGAGC  
 GAGCTTCTGGCTAACGGCCTCGTCCTGCTCCTGAACTCGCTGGGCGTCTC  
 AGCGATAAACGTCCGCCACGACAGCGGGGTTTACAGGGTCTACGTGAACG  
 AGGAACTGCCCTTTACAGAGTACCGGAAGCGGAAGAACGCCTCACTTACT  
 CCCACGTCATACCGAGGGAAGTGCTGGAGGAGACTTCGGCCGGGCCTTCC  
 AGAAGAACATGAGTCACGGGAAATTCAGGGAGCTGGTGAAAGCGGGGAG  
 CTCGACGCGGAAAGGGCCGGTAGGATAGGCTGGCTCCTCGACGGGGATAT  
 AGTCCTCGACAGGTCTCGGAAGTCAGGAAGGAAAGCTACGAGGGGTACG  
 TCTACGACCTGAGCGTTGAGGAGGACGAGAACTTCTGGCGGGCTTTGGGT  
 TCCTCTACGCGCACAACNN

FIG. 4 (cont.)

6/20

AGCTACTACGGCTACTACGGCTATGCCAGGG  
CAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGG  
GAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTAA  
AGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCCTGGAGCGG  
ACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTCTTAAACTATATCAAT  
CCCAAAC TGCCCGGCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAG  
GGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCA  
AGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATA  
GCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGA Extein 2  
CGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCA  
AGTACGAGGTTCGCGCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGC  
GAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGCG  
TTTGGCCGCCAGAGGTGTAAAAATCCGGCCCGAACTGTGATAAGCTACA  
TCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGAC  
  
GAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAA  
CCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCA  
AGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTGGGGCTTGGCGCGTGG  
CTGAAGCCGAAGGGGAAGAAGAAGTGA

GGAATTATCTGGTTTCTTTTCCC  
AGCATTAATGCTTCCGACATTGCCTTATTTATGAAATCCTGTTGTGCC  
TGAGTTTGTGCCAGAAAACAGCCTGTTCTGACGGCGCTTTTCTTGCCAG  
GTCTCTTGAGTTTCGCAAGGGTCTTCTCGACCAGCTCAATGGTCTTGTCC  
TCATTGTTTNNNNNNNNNNNNNNNNNNNNCCGGGGACTTCATACTGGC  
GGTAATAGACAGGGATTCCCTTCCTCAAGGACTTCCCGGAGGCATTGGAG  
TTTTTTGGTGGGGCTTTCACAGGATTTGCTCATCTTGTGGATTTCTCGTT  
CGATTGAATCTGTCCACTTGAGGGTGTAGGTCGAGACGGTGGAGCGCGTA  
TTCCGGGAGCGGGTCTTGAGGCTCCATTTTTCAGTCCCTCCGGCGAAG 3' Untranslated sequence  
AAGTGAACTCAAGCCGGGTGTTAGCTTATGTTATGTTCCCAACTCCTCC  
AGCACCTCCAGGATCCCCCAATCCCGGAACCTCGAAGCCCTCTCGTGG  
ATCTTTCTAACTTCCTCTGCCTCCGGGTTTATCCAGACCGCCACATGCC  
GGCTCTCAGCGCACCTCGAAATCCTCCGCGTAGGTGTCGCCGATGTGGA  
TTGCCCTCGTCCGGCTCGACCCCGAAGCATCGAGCGGTTTTCTGAACATCT  
CGGGCATCGGCTTATACGCCAGAACCCTCGTCGGCGAAGAAGGTTCCCTCA  
ATGTAGTCCATCAGGCCGAACCTCTCGAGGGGGGGCCGGTACCCAATTC  
GCCCTATAGTGAGTCGATTACAATTCAGTGGCCGTCGTTTTACAACGTCG  
TGA CTGGGAAAACCTGGCGTTACCCAACCTAAGTCGCTTTCAGCACAT  
CCCCC

FIG. 4 (cont.)

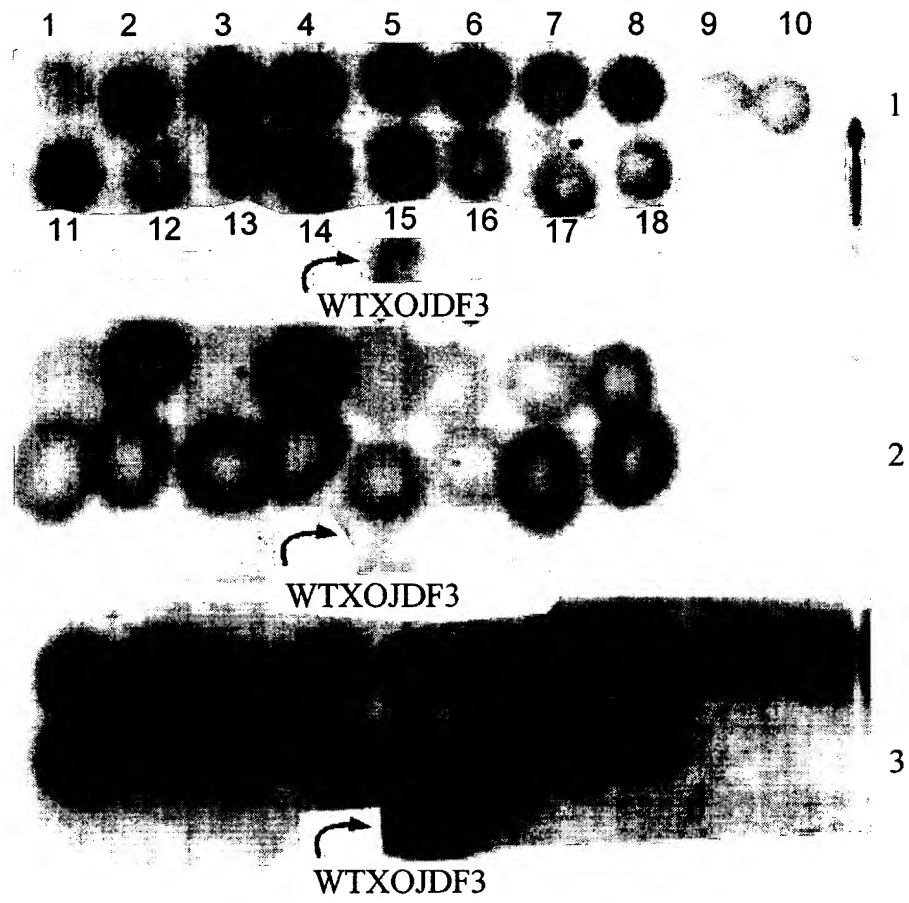


FIG. 5

Sequencing with Purified Mutants

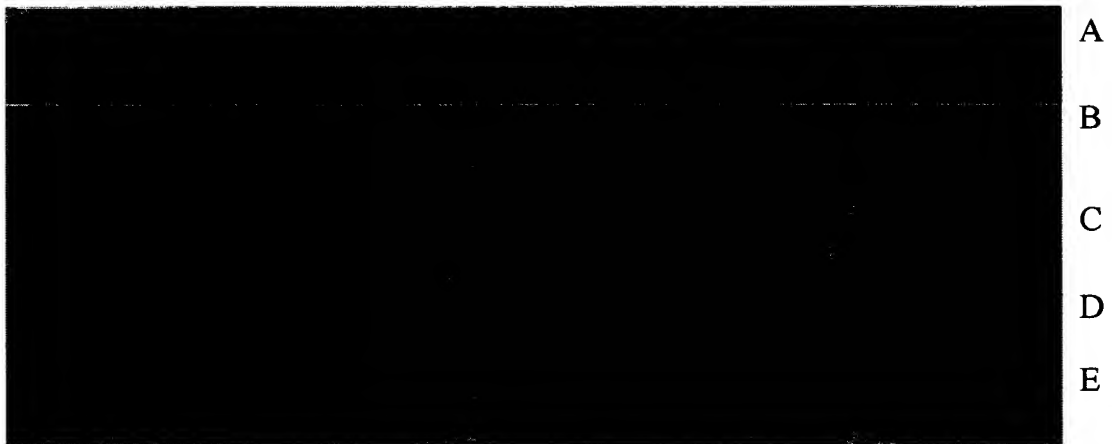


FIG. 6

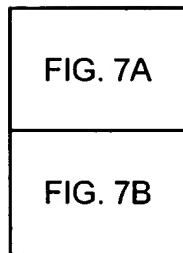


FIG. 7



Sequencing with Dye-labeled Dideoxynucleotides



9/20

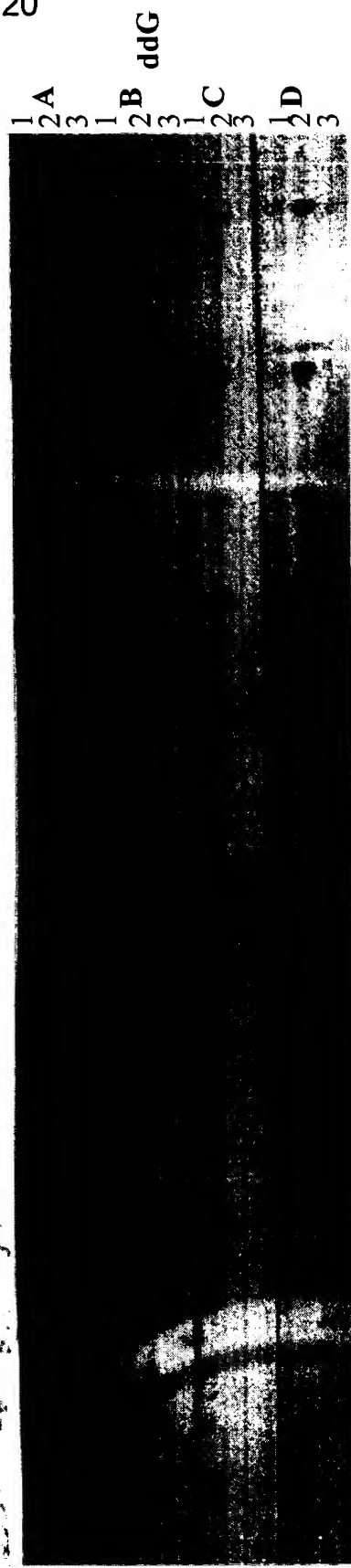


FIG. 7A

1A  
2  
3  
1B ddC  
2  
3  
1C  
2  
3  
1D  
2  
3



10/20

1A  
2  
3  
1B ddT  
2  
3  
1C  
2  
3  
1D  
2  
3

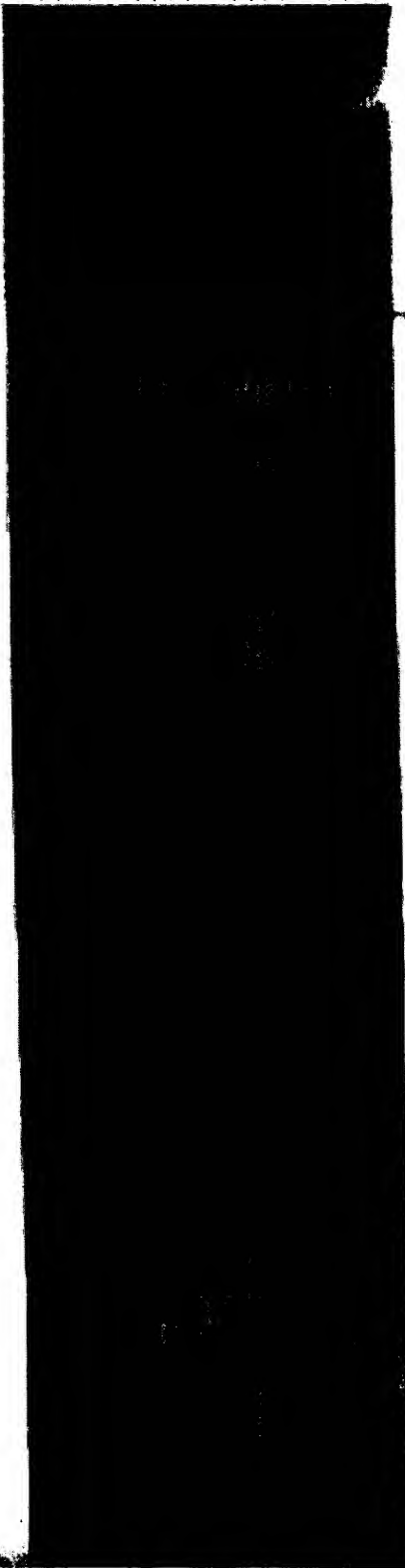


FIG. 7B

Sequencing with the P410L, A485T Double Mutant and  $\alpha$ - $^{33}\text{P}$  Dideoxynucleotides



FIG. 8

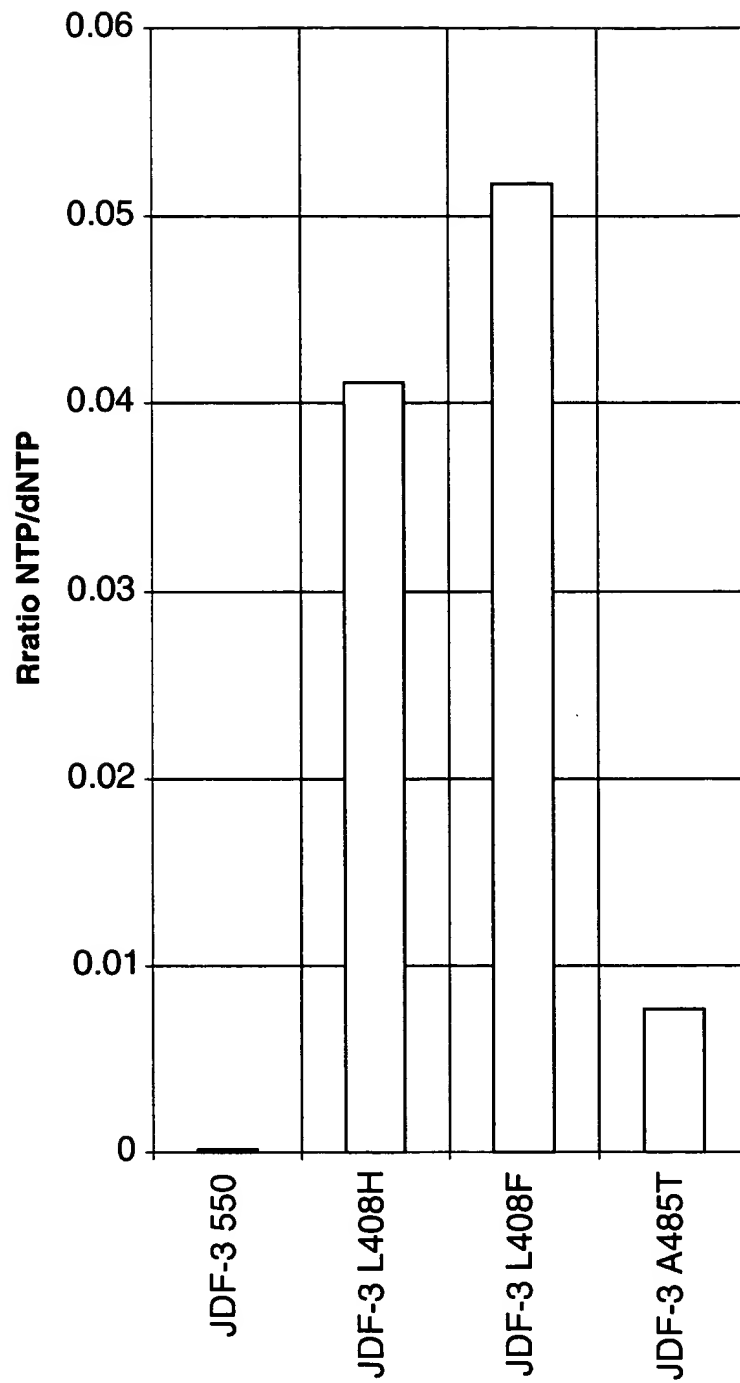
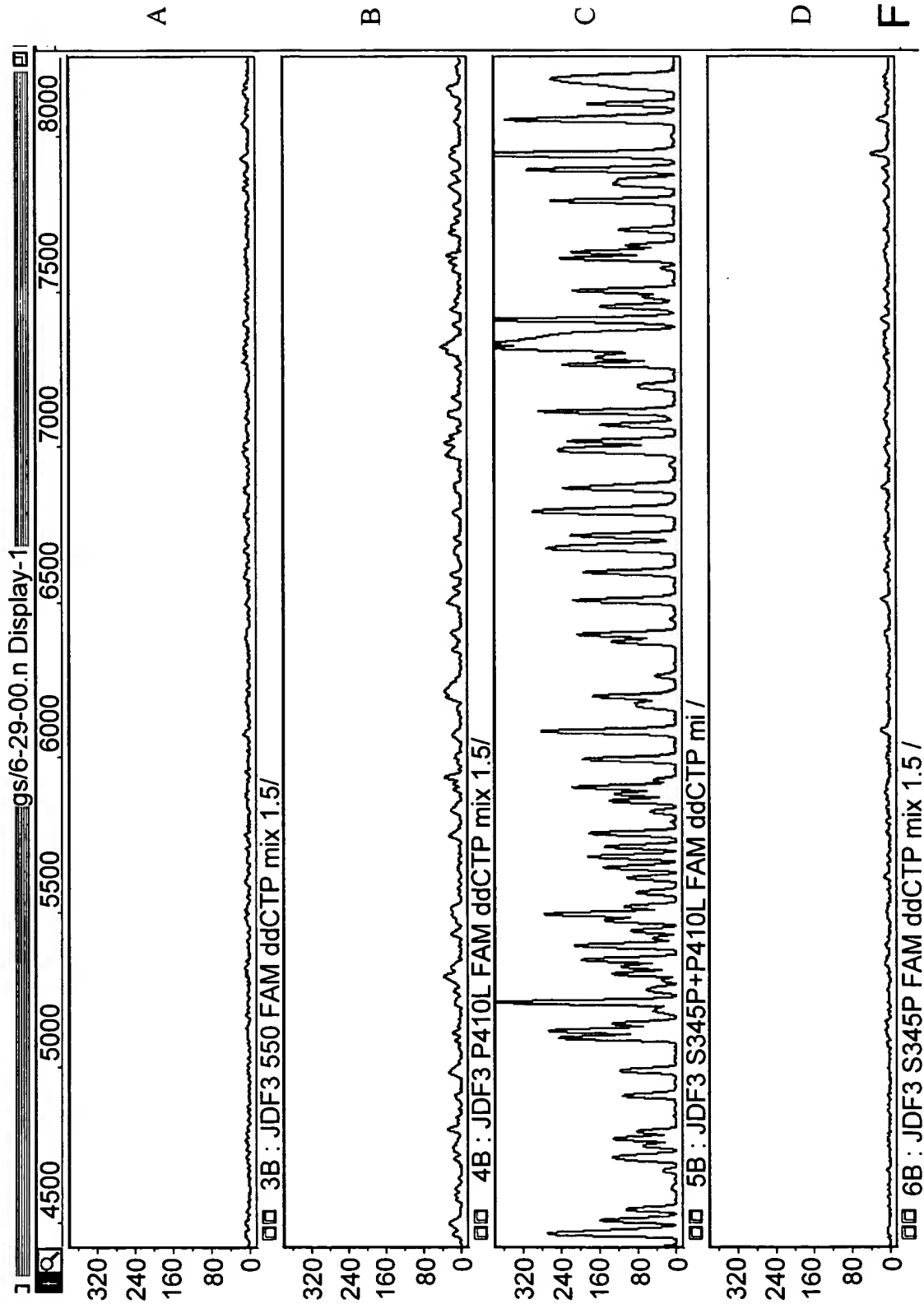


FIG. 9



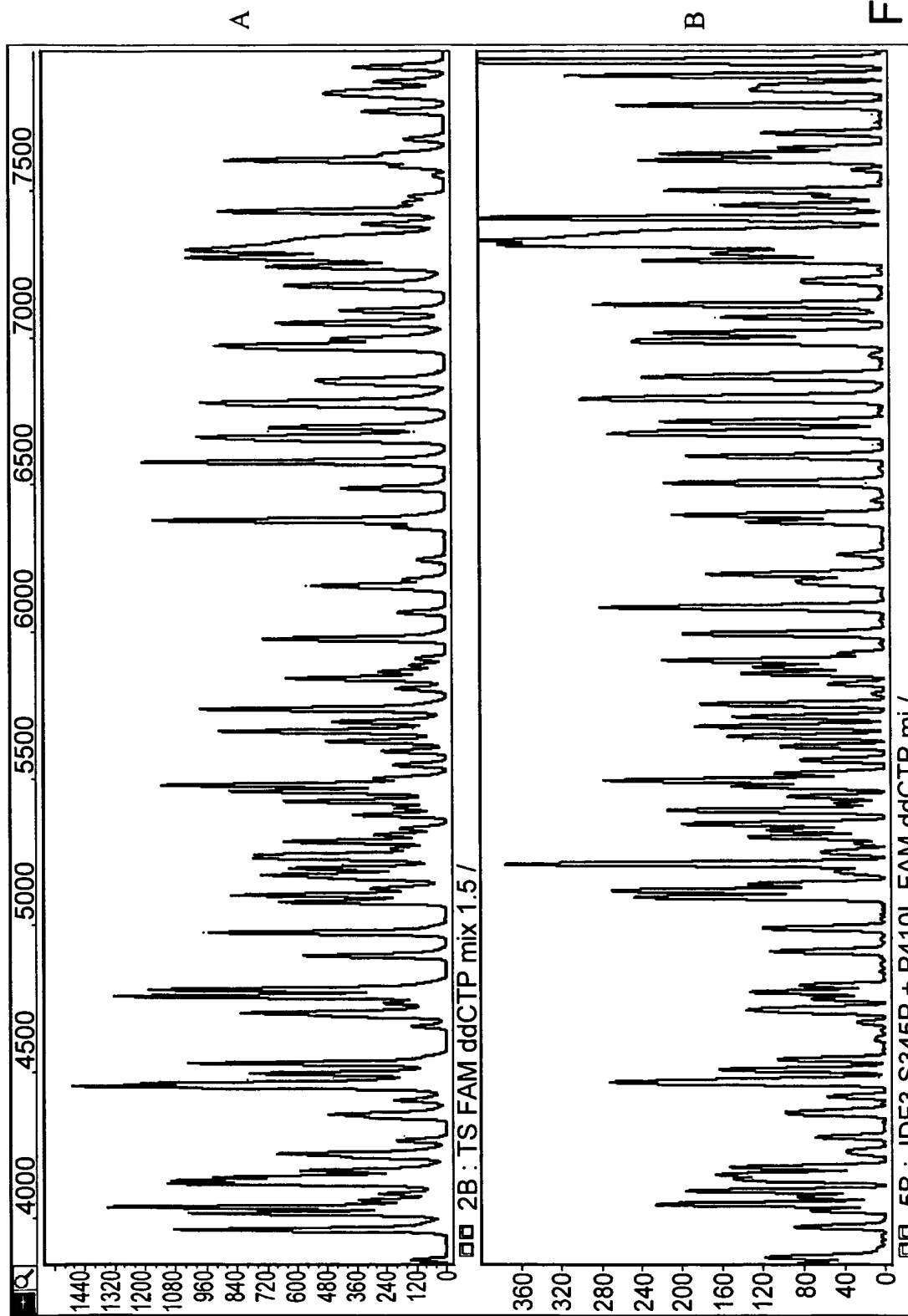


FIG. 11

**<sup>33</sup>P**-TAACGTTGGGGGGGCA →  
 TGCAACCCCCCGTAT

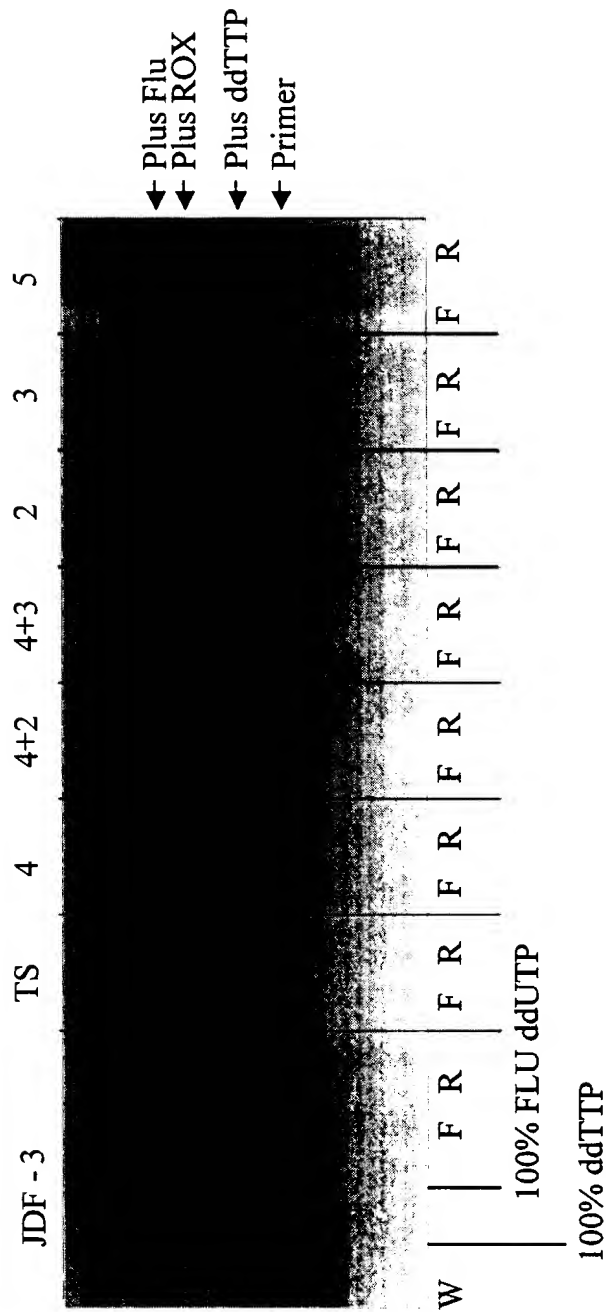
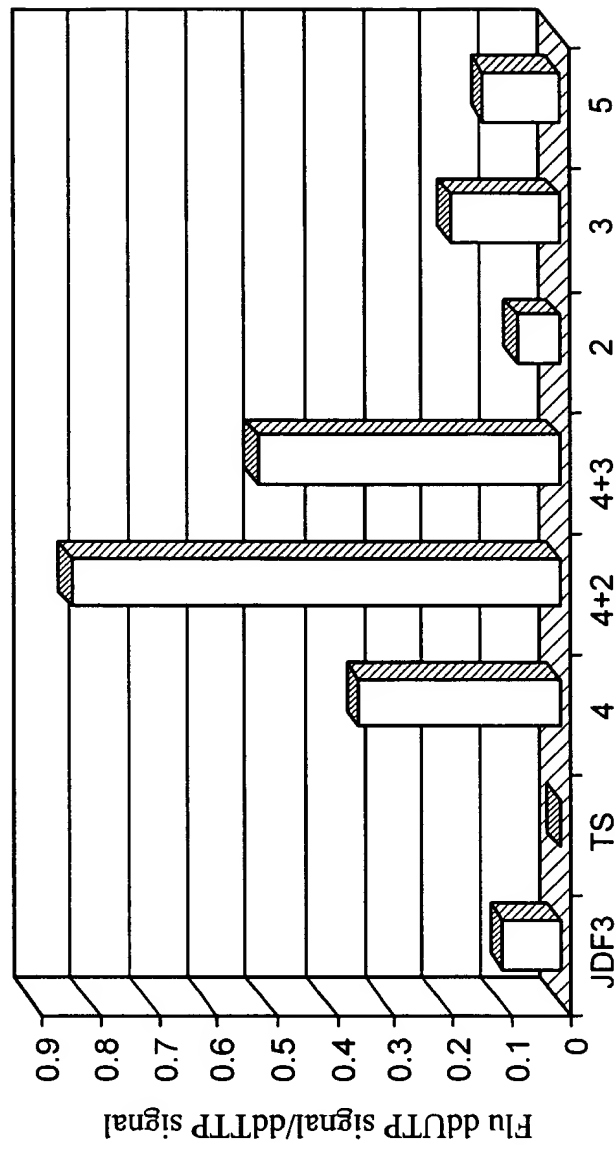


FIG. 12



Mutants

FIG. 13



```

4      1  -----LVXNAXSTGNLVEWFLLRK
10     1  -----VWDVSRSTGNLVERFLLRK
13     1  -----VWDVSRSTGNLVEWFLLRK
16     1  -----VWDVSRSTGNLVEWFLLRK
18     1  -----VWDVSRSTGNLVEWFLLRK
19     1  -----VWDVXRSTGNLVEWFLLRK
28     1  -----VWDVPRSTGNLVEWFLLRK
34     1  -----VWDVSRSTGNLVEWFLLRK
41     1  -----VWDVSRSTGNLVEWFLLRK
33     1  -----VWDVSRSTGNLVEWFLLRK
48     1  -----YWSXPXLRTGNLVEWFLLRK
55     1  -----VLGTXPSTGNLVEWFLLRK
64     1  -----XXXFWDVSRSTGNLVEWFLLRK
Jdf3  301 TGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRK
          310      320      330      340      350      360

4      20 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
10     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHSVSP
13     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
16     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
18     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
19     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGQWDNIA_YLDFRSLYPSIIITHNVSP
28     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
34     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
41     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGPWDNIVYLDFRSLYPSIIITHNVSP
33     21 AYERNKLAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
48     21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
55     22 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSHYPSIIITHNVSP
64     24 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
Jdf3  361 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
          370      380      390      400      410      420

```

FIG. 14

4 80 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 10 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 13 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 16 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 18 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 19 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 28 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 34 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 41 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 33 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 48 81 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 55 82 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 64 84 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 Jdf3 421 DTLNREGCRSYDVAPEVGHKFKDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD  
 430 440 450 460 470 480

FIG. 14 (cont.)

4 140 YRQRAIKILANSYYGYCGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 10 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 13 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 16 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 18 141 YRQRAIKILANYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 19 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 28 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 34 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 41 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 33 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 48 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 55 142 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 64 144 YRQRAIKILANSYYGNYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 Jdf3 481 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD

490 500

4 200 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 10 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 13 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 16 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELKYEGFYVRGFFVTKKKYAVIDEE  
 18 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 19 201 TDGLHATIPGADAETVKKKAMEFLNYINLKLPGLELEYEGFYVRGFFVTKKKXAVIDEE  
 28 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 34 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 41 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 33 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLEPEYEGFYVRGFFVTKKKYAVIDEE  
 48 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 55 202 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 64 204 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 Jdf3 541 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE

550 560 570 580 590 600

FIG. 15

4 260 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL  
 10 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEEL  
 13 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVRKVTEKLSKYEVPPPEKL  
 16 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL  
 18 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHDDVEEAVRIVREVTEKLSKYEVPPPEKL  
 19 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAIRIVREVTEKLSKYEVPPPEKL  
 28 261 GKIATRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL  
 34 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLNKYEVPPPEKL  
 41 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL  
 33 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL  
 48 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPVKL  
 55 262 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPGGEA  
 64 264 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL  
 Jdf3 601 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL  
 610 620 630 640 650 660

FIG. 15 (cont.)

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**